RAW SEQUENCE LISTING
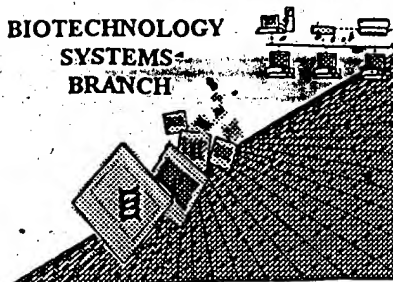# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/965536_

Source: _OIPE_

Date Processed by STIC: _11/07/01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/965536

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length.

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represe any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 11/07/2001
PATENT APPLICATION: US/09/965,536   TIME: 14:48:12

Input Set : **A:\30534111.app**
Output Set: **N:\CRF3\11072001\I965536.raw**

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 3 <110> APPLICANT: FEDER, J. N.
 4        MINTIER, G.
 5        RAMANATHAN, C. S.
 6        HAWKEN, D. R.
 8 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY5,
 9        EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
11 <130> FILE REFERENCE: DOO41NP/3053-4118US3
13 <140> CURRENT APPLICATION NUMBER: US/09/965,536
14 <141> CURRENT FILING DATE: 2001-09-26
16 <150> PRIOR APPLICATION NUMBER: 60/235,713
17 <151> PRIOR FILING DATE: 2000-09-27
19 <150> PRIOR APPLICATION NUMBER: 60/261,781
20 <151> PRIOR FILING DATE: 2001-01-16
22 <150> PRIOR APPLICATION NUMBER: 60/306,605
23 <151> PRIOR FILING DATE: 2001-07-19
25 <150> PRIOR APPLICATION NUMBER: 60/310,436
26 <151> PRIOR FILING DATE: 2001-08-03
28 <160> NUMBER OF SEQ ID NOS: 61
30 <170> SOFTWARE: PatentIn Ver. 2.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 2214
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <400> SEQUENCE: 1
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40 tgcttacccc gagcttttca ctgtgatggc aaggatgact gtgggaacgg ggcggacgaa 180
41 gagaactgtg gtgacactag tggatgggcg accatatttg gcacagtgca tggaaatgct 240
42 aacagcgtgg ccttaacaca ggagtgcttt ctaaaacagt atccacaatg ctgtgactgc 300
43 aaagaaactg aattggaatg tgtaaatggt gacttaaagt ctgtgccgat gatttctaac 360
44 aatgtgacat tactgtctct taagaaaaac aaaatccaca gtcttccaga taaagttttc 420
45 atcaaataca caaaacttaa aaagatattt cttcagcata attgcattag acacatatcc 480
46 aggaaagcat tttttggatt atgtaatctg caaatattat atctcaacca caactgcatc 540
47 acaaccctca gacctggaat attcaaagac ttacatcagc taacttggct aattctagat 600
48 gacaatccaa taaccagaat ttcacagcgc ttgtttacgg gattaaattc cttgtttttc 660
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50 caactcaact gggtggattt ggaaggcaat agaataaagt atctcacaaa ttctacgttt 780
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56 aatctttctc acatttattt caaaaacttt cgatactgct cctatgctcc ccatgtccga 1140
57 atatgtatgc ccttgacgga cggcatttct tcatttgagg acctcttggc taacaatatc 1200
58 ctcagaatat ttgtctgggt tatagctttc attacctgct ttggaaatct ttttgtcatt 1260
59 ggcatgagat ctttcattaa agctgaaaat acaactcacg ctatgtccat caaaatcctt 1320
60 tgttgtgctg attgcctgat gggtgtttac ttgttctttg ttggcatttt cgatataaaa 1380
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RAW SEQUENCE LISTING   DATE: 11/07/2001
PATENT APPLICATION: US/09/965,536   TIME: 14:48:12

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Output Set: N:\CRF3\11072001\I965536.raw

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63 ttggagaagt tcctggtcat tgtcttcccc ttcagtaaca ttcgacctgg aaaacggcag 1560
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65 tggaataagg attattttgg aaacttttat gggaaaaatg gagtatgttt cccactttat 1680
66 tatgaccaaa cagaagatat tggaagcaaa gggtattctc ttggaatttt cctaggtgtg 1740
67 aacttgctgg ctttttctcat cattgtgttt tcctatatta ctatgttctg ttccattcaa 1800
68 aaaaccgcct tgcagaccac agaagtaagg aattgttttg gaagagaggt ggctgttgca 1860
69 aatcgtttct tttttatagt gttctctgat gccatctgct ggattcctgt atttgtagtt 1920
70 aaaatccttt ccctcttccg ggtggaaata ccagacacaa tgacttcctg gatagtgatt 1980
71 ttttttccttc cagttaacag tgctttgaat ccaatcctct atactctcac aaccaacttt 2040
72 tttaaggaca agttgaaaca gctgctgcac aaacatcaga ggaaatcaat tttcaaaatt 2100
73 aaaaaaaaaa gtttatctac atccattgtg tggatagagg actcctcttc cctgaaactt 2160
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78 <211> LENGTH: 737
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 2

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86  Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr
87              20                  25                  30
89  Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
90          35                  40                  45
92  Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
93      50                  55                  60
95  Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala
96  65                  70                  75                  80
98  Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln
99              85                  90                  95
101 Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu
102             100                 105                 110
104 Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys
105         115                 120                 125
107 Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr
108         130                 135                 140
110 Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser
111 145                 150                 155                 160
113 Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn
114             165                 170                 175
116 His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His
117             180                 185                 190
119 Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser
120         195                 200                 205
122 Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val
123     210                 215                 220
125 Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro
126 225                 230                 235                 240
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RAW SEQUENCE LISTING   DATE: 11/07/2001
PATENT APPLICATION: US/09/965,536   TIME: 14:48:12

Input Set : A:\30534111.app
Output Set: N:\CRF3\11072001\I965536.raw

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129             245             250             255
131 Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu Pro
132             260             265             270
134 Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys
135         275             280             285
137 Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser
138         290             295             300
140 Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu Ser
141 305             310             315             320
143 Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu Lys
144             325             330             335
146 Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Asn
147             340             345             350
149 Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys
150         355             360             365
152 Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met Pro
153     370             375             380
155 Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn Ile
156 385             390             395             400
158 Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly Asn
159             405             410             415
161 Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr
162         420             425             430
164 His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly
165         435             440             445
167 Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly Gln
168     450             455             460
170 Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg Leu
171 465             470             475             480
173 Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu Leu
174             485             490             495
176 Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser
177         500             505             510
179 Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys Ile
180         515             520             525
182 Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys Asp
183     530             535             540
185 Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr
186 545             550             555             560
188 Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly Ile
189             565             570             575
191 Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser Tyr
192         580             585             590
194 Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu
195         595             600             605
197 Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val Ala Asn Arg Phe Phe
198     610             615             620
200 Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val
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RAW SEQUENCE LISTING   DATE: 11/07/2001
PATENT APPLICATION: US/09/965,536   TIME: 14:48:12

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Output Set: N:\CRF3\11072001\I965536.raw

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203 Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr Ser
204               645                  650                  655
206 Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile
207               660                  665                  670
209 Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu
210           675                  680                  685
212 Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser
213       690                  695                  700
215 Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu
216 705                  710                  715                  720
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228 <213> ORGANISM: Homo sapiens
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235 <211> LENGTH: 1026
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
239 <400> SEQUENCE: 4
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241 agatgacatc tgcaatgctt ttcatcttta ccaacggcaa gcctttctgc acagagagca 120
242 cagcagaatg gctcctgtca ctgcattcca atggcagctg tactatctac caaccgtgct 180
243 gaggacagca ccaaaggttc ctctcctcac cccacatgcc tgaaaagcac atgtgaattc 240
244 gtgtatagtg ggctgaggtg cagctgatct ctagctaatc aacacaaccc accaacaaat 300
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248 aaaatattca tctacccgaa gtcctcctct gtgaaggccg gtggagtagc cactttgaaa 540
249 acagaacttc caaccaggtt accatgtcta acctatgacc agagagtcac actgatgaag 600
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252 ctttaatatt cttaaagtat aatttcttta gagcagtatc cctattgctg gcaagttctg 780
253 ctttcataaa atatgcagat aagaagtgtt aaatgggatt caagaattat ggttttattt 840
254 gggactgttt gcatactcac aatggttttg ttctcattgt ttttaacaaa aaagcaatga 900
255 agtttggggt ggttttttga aaacgaaact gaaaaaaatt atatgtgaaa atgagaactg 960
256 ggtaaataaa attatatttt gcaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
257 aaaaag                                                          1026
260 <210> SEQ ID NO: 5
261 <211> LENGTH: 2142
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo sapiens
265 <400> SEQUENCE: 5
266 atgttctttc tacttcattt catcgttctg atcaatgtca aagattttgc actgactcaa 60
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267 ggtagcatga tcactccttc atgccaaaaa ggatattttc cctgtgggaa tcttaccaag 120
268 tgcttacccc gagcttttca ctgtgatggc aaggatgact gtgggaacgg ggcggacgaa 180
269 gagaactgtg gtgacactag tggatgggcg accatatttg gcacagtgca tggaaatgct 240
270 aacagcgtgg ccttaacaca ggagtgcttt ctaaaacagt atccacaatg ctgtgactgc 300
271 aaagaaactg aattggaatg tgtaaatggt gacttaaagt ctgtgccgat gatttctaac 360
272 aatgtgacat tactgtctct taagaaaaac aaaatccaca gtcttccaga taaagttttc 420
273 atcaaataca caaaacttaa aaagatattt cttcagcata attgcattag acacatatcc 480
274 aggaaagcat tttttggatt atgtaatctg caaatattaa ttctagatga caatccaata 540
275 accagaattt cacagcgctt gtttacggga ttaaattcct tgttttttcct gtctatggtt 600
276 aataactact tagaagctct tcccaagcag atgtgtgccc aaatgcctca actcaactgg 660
277 gtggatttgg aaggcaatag aataaagtat ctcacaaatt ctacgtttct gtcgtgcgat 720
278 tcgctcacag tgctgtttct gcctagaaat caaattggtt ttgttccaga gaagacattt 780
279 tcttcattaa aaaatttagg agaactggat ctgtctagca atacgataac ggagctatca 840
280 cctcaccttt ttaaagactt gaagcttcta caaaagctga acctgtcatc caatcctctt 900
281 atgtatcttc acaagaacca gtttgaaagt cttaaacaac ttcagtctct agacctggaa 960
282 aggatagaga ttccaaatat aaacacacga atgtttcaac ccatgaagaa tctttctcac 1020
283 atttatttca aaaactttcg atactgctcc tatgctcccc atgtccgaat atgtatgccc 1080
284 ttgacggacg gcatttcttc atttgaggac ctcttggcta acaatatcct cagaatattt 1140
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291 ctcatttgca tctggatggc gggattttta atagctgtaa ttccatttg gaataaggat 1560
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294 tttctcatca ttgtgttttc ctatattact atgttctgtt ccattcaaaa aaccgccttg 1740
295 cagaccacag aagtaaggaa ttgtttttgga agagaggtgg ctgttgcaaa tcgtttctttt 1800
296 tttatagtgt tctctgatgc catctgctgg attcctgtat ttgtagttaa aatcctttcc 1860
297 ctcttccggg tggaaatacc agacacaatg acttcctgga tagtgatttt tttccttcca 1920
298 gttaacagtg ctttgaatcc aatcctctat actctcacaa ccaactttt taaggacaag 1980
299 ttgaaacagc tgctgcacaa acatcagagg aaatcaattt tcaaaattaa aaaaaaaagt 2040
300 ttatctacat ccattgtgtg gatagaggac tcctcttccc tgaaacttgg ggttttgaac 2100
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305 <211> LENGTH: 713
306 <212> TYPE: PRT
307 <213> ORGANISM: Homo sapiens
309 <400> SEQUENCE: 6
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314              20                 25                 30
316 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
317          35                 40                 45
319 Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
320      50                 55                 60
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<210> 29
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Oligo 1;
      N=A+G+C+T;  K=C+G+T

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nnknnknnkn nknnknnknn knnkccgggt ccgggcggc                       99


<210> 30
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Oligo 2;
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aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nvnnvnnvnn gccgcccgga cccgg                           95
```

**Does Not Comply
Corrected Diskette Needed**

*Must enumerate unknown "n's" in
Fields 221, 222 and 223.*

met

*Fields 221 and 222 must be included in addition
to fields 223. Unknowns must be enumerated as
follows: "unsure", some numeric location, and some
possible value.*

*Notation is odd. Do you mean
more clearly That N = A or G or C or T*

VERIFICATION SUMMARY　　　　　　　　DATE: 11/07/2001
PATENT APPLICATION:　**US/09/965,536**　　TIME: 14:48:13

Input Set : **A:\30534111.app**
Output Set: **N:\CRF3\11072001\I965536.raw**

```
L:13   M:270 C: Current Application Number differs, Replaced Current Application Number
L:1767 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:1767 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1768 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:1768 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:1768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1781 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1781 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1782 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1782 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
```